

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:48:41 ; Search time 2351.15 Seconds

(without alignments)
161.385 Million cell updates/sec

Title: US-09-851-670-15

Perfect score: 23
Sequence: 1 aacgtgtcgcgtctcagagaca 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
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14: gb_vl:*
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16: em_fun:*
17: em_hum:*
18: em_in:*
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21: em_ov:*
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24: em_pl:*
25: em_ro:*
26: em_sts:*
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28: em_un:*
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31: em_htgo_inv:*
32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14.6	63.5	48	9	S56760	S56760 BCL2 {fragm
2	13.4	58.3	55	10	S77019	S77019 c-myc...Ig
3	13	56.5	28	6	AX034687	AX034687 Sequence
4	13	56.5	57	6	AR009400	AR009400 Sequence
5	13	56.5	58	10	AF557324	AF557324 Mus muscu
6	12.8	55.7	24	6	A08385	A08385 Synthetic D
7	12.8	55.7	27	6	A08384	A08384 Synthetic D
8	12.8	55.7	27	6	AX069493	AX069493 Sequence
9	12.8	55.7	27	6	AX069494	AX069494 Sequence
10	12.8	55.7	59	5	U33690	U33690 Hypentelium
11	12.6	54.8	51	6	AX159789	AX159789 Sequence
12	12.6	54.8	60	6	AR118184	AR118184 Sequence
13	12.6	54.8	60	6	I01529	I01529 Sequence 4
14	12.4	53.9	35	6	E07618	E07618 PCR primer
15	12.4	53.9	43	6	AR079998	AR079998 Sequence
16	12.4	53.9	43	6	AR085924	AR085924 Sequence
17	12.4	53.9	43	6	AR093310	AR093310 Sequence
18	12.4	53.9	43	6	AR121680	AR121680 Sequence
19	12.4	53.9	44	6	AR043085	AR043085 Sequence
20	12.4	53.9	49	6	AX082373	AX082373 Sequence
21	12.2	53.0	18	12	AB069089	AB069089 Synthetic
22	12.2	53.0	19	6	I88029	I88029 Sequence 7
23	12.2	53.0	21	6	AX092795	AX092795 Sequence
24	12.2	53.0	23	6	A99258	A99258 Sequence 34
25	12.2	53.0	24	6	A99252	A99252 Sequence 28
26	12.2	53.0	42	6	A36507	A36507 Sequence 48
27	12.2	53.0	42	6	AR080140	AR080140 Sequence
28	12.2	53.0	49	6	AR047941	AR047941 Sequence
29	12.2	53.0	51	6	AX162776	AX162776 Sequence
30	12.2	53.0	59	6	AR031474	AR031474 Sequence
31	12.2	52.2	26	6	AX038002	AX038002 Sequence
32	12.2	52.2	37	6	AX008530	AX008530 Sequence
33	12.2	52.2	38	6	AX008531	AX008531 Sequence
34	12.2	52.2	41	6	AR050326	AR050326 Sequence
35	12.2	52.2	46	6	AR043084	AR043084 Sequence
36	12.2	52.2	50	6	AX157364	AX157364 Sequence
37	12.2	52.2	51	6	AX157786	AX157786 Sequence
38	12.2	52.2	51	6	AX165195	AX165195 Sequence
39	12.2	52.2	52	6	AR062114	AR062114 Sequence
40	12	52.2	60	1	S38798	S38798 (Junction J
41	11.8	51.3	21	6	AR020925	AR020925 Sequence
42	11.8	51.3	21	6	AR020927	AR020927 Sequence
43	11.8	51.3	21	6	AR020928	AR020928 Sequence
44	11.8	51.3	21	6	AR051048	AR051048 Sequence
45	11.8	51.3	21	6	AR051050	AR051050 Sequence

ALIGNMENTS

RESULT	1	
LOCUS	S56760	48 bp DNA
DEFINITION	BCL2 {fragment 2, translocation breakpoint, variant cluster region}	PRI 22-JUL-1993
ACCESSION	S56760	[human, peripheral blood cells, Genomic, 48 nt].
VERSION	S56760.1	GI:299253
KEYWORDS		
SOURCE	human peripheral blood cells.	
ORGANISM	Homo sapiens	
REFERENCE	Seite,P., Leroux,D., Hillion,J., Montell,M., Berger,R.,	
AUTHORS	Mathieu-Manuil,D. and Larsen,C.J.	
TITLE	Molecular analysis of a variant 18:22 translocation in a case of	
JOURNAL	Lymphocytic lymphoma	
MEDLINE	Genes Chromosomes Cancer 6 (1), 39-44 (1993)	
REMARK	Genbank staff at the National Library of Medicine created this	

entry [NCBI g1bbsq 127183] from the original journal article.
This sequence comes from Fig. 3.
Map location: t(18;22).

FEATURES

source
1..48
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..48
/partial
/gene="BCL2"
BASE COUNT 7 a 10 c 22 g 9 t
ORIGIN

Query Match 63.5%; Score 14.6; DB 9; Length 48;
Best Local Similarity 81.0%; Pred. No. 1e+04;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 cgtgtcggtcctcagagaca 23
11 11 11 11 11 11 11 11
Db 20 CCGGTGGGCTGTCGAGACA 40

RESULT 2

S77019 55 bp DNA ROD 27-JUL-1995
LOCUS c-myc. : Ig gamma-2b (translocation) [mlce, transgenic, genomic, 3
DEFINITION genes, 55 nt].
ACCESSION S77019
VERSION S77019.1 GI:913974
KEYWORDS
SOURCE Mus sp. transgenic.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 55)
AUTHORS Martin, M.C., Hsu, B., Stephens, L.C., Britsday, S. and McDonnell, T.J.
TITLE The functional basis of c-myc and bcl-2 complementation during
multistep lymphomagenesis in vivo
JOURNAL Exp. Cell Res. 217 (2), 240-247 (1995)
MEDLINE 95212436
REMARK

Genbank staff at the National Library of Medicine created this
entry [NCBI g1bbsq 163932] from the original journal article.
This sequence comes from Fig. 1.
Map location: t(12;15).

FEATURES

source
1..55
/organism="Mus sp."
/db_xref="taxon:10095"
1..24
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/gene="c-myc"
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/partial
/gene="c-myc"
/gene="c-myc-Ig gamma 2b"
/note="fusion gene"
29..55
/partial
/gene="Ig gamma-2b"
BASE COUNT 15 a 15 c 15 g 10 t
ORIGIN

Query Match 58.3%; Score 13.4; DB 10; Length 55;
Best Local Similarity 73.9%; Pred. No. 4.2e+04;

Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 aacgtgctgctcctcagagaca 23
11 11 11 11 11 11 11 11
Db 30 AACGCTCAGGCTCTAAGAGACA 52

RESULT 3

AX034687 28 bp DNA PAT 15-NOV-2000
LOCUS AX034687
DEFINITION Sequence 24 from Patent EP1035206.
ACCESSION AX034687
VERSION AX034687.1 GI:11190661
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequence.

REFERENCE 1 (bases 1 to 28)
AUTHORS Hoshino, T., Ojima, K. and Setoguchi, Y.
TITLE Astaxanthin synthetase
JOURNAL Patent: EP 1035206-A 24 13-SEP-2000;
HOFFMANN LA ROCHE (CH)
location/Qualifiers

FEATURES

source
1..28
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="antisense primer for construction of TPI terminator
cassette"
BASE COUNT 6 a 9 c 9 g 4 t
ORIGIN

Query Match 56.5%; Score 13; DB 6; Length 28;
Best Local Similarity 76.2%; Pred. No. 7.5e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 cgtgtcggtcctcagagaca 23
11 11 11 11 11 11 11 11
Db 7 CGTGGCGAGTCGACGAGACA 27

RESULT 4

AR009400 57 bp DNA PAT 04-DEC-1998
LOCUS AR009400
DEFINITION Sequence 168 from patent US 5756291.
ACCESSION AR009400
VERSION AR009400.1 GI:3968205
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 57)
AUTHORS Griffin, L., Albrecht, G., Latham, J., Leung, L., Vermaas, E. and
Toole, J.J.
TITLE Aptamers specific for biomolecules and methods of making
JOURNAL Patent: US 5756291-A 168 26-MAY-1998;
location/Qualifiers

FEATURES
source
1..57
/organism="unknown"
BASE COUNT 10 a 10 c 22 g 9 t 6 others
ORIGIN

Query Match 56.5%; Score 13; DB 6; Length 57;
Best Local Similarity 76.2%; Pred. No. 6.8e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 cgtgtcggtcctcagagaca 23
11 11 11 11 11 11 11 11
Db 9 CCGATCGGCTGTCACAGACA 29

RESULT 5

AF357324 58 bp RNA ROD 06-JUN-2001
LOCUS AF357324
DEFINITION Mus musculus clone MBL1-142 C/D box snRNA, partial sequence.
ACCESSION AF357324
VERSION AF357324.1 GI:14276919
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 58)
AUTHORS Huttenhofer,A., Kieffmann,M., Meier-Ewert,S., O'Brien,J.,
Lehrach,H., Bachelierle,J.-P. and Brosius,J.
TITLE RNCmics: an experimental approach that identifies 201 candidates
for novel, small, non-messenger RNAs in mouse
JOURNAL EMBO J. 20 (11), 2943-2953 (2001)
PUBMED 11387227
REFERENCE 2 (bases 1 to 58)
AUTHORS Huttenhofer,A., Kieffmann,M., Meier-Ewert,S., O'Brien,J.,
Lehrach,H., Bachelierle,J.-P. and Brosius,J.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-2001) Institute of Experimental Pathology /
Molecular Neurobiology, ZMBE, University of Muenster,
Von-Esmarch-Str. 56, Muenster D-48149, Germany

FEATURES
source Location/Qualifiers
1..58
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="MBII-142"
misc_RNA
1..38
/note="missing at least 5-10 bases"
/product="C/D box snRNA: small non-messenger RNA
(snmRNA)"

BASE COUNT 14 a 13 c 20 g 11 t

ORIGIN

Query Match 56.5%; Score 13; DB 10; Length 58;
Best Local Similarity 76.2%; Pred. No. 6.7e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 acgtgtgcggtcctcagagac 22
||||| || ||| |||||
DB 10 ACGTGCTGGCCACTGAGAC 30

RESULT 6
A08385/c A08385 24 bp DNA PAT 26-AUG-1993
LOCUS A08385
DEFINITION Synthetic DNA sequence for primate prolinsulin, Reverse complement.
ACCESSION A08385
VERSION A08385.1 GI:411636
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 24)
AUTHORS Doerschug,M.
TITLE Insulin derivatives, their use and a pharmaceutical composition
JOURNAL containing same
PATENT: EP 0368187-A 8 16-MAY-1990;
HOECHST AKTIENGESellschaft
FEATURES
source Location/Qualifiers
1..24
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 5 a 5 c 9 g 5 t

ORIGIN

Query Match 55.7%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 9.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 acgtgtgcggtcctca 17
||||| ||||| |||||
DB 17 ACCTGTGCGGTCTCA 2

RESULT 7
A08384

LOCUS A08384 27 bp DNA PAT 26-AUG-1993
DEFINITION Synthetic DNA sequence for primate prolinsulin.
ACCESSION A08384
VERSION A08384.1 GI:413447
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 27)
AUTHORS Doerschug,M.
TITLE Insulin derivatives, their use and a pharmaceutical composition
JOURNAL containing same
PATENT: EP 0368187-A 7 16-MAY-1990;
HOECHST AKTIENGESellschaft
FEATURES
source Location/Qualifiers
1..27
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 6 a 10 c 5 g 6 t

ORIGIN

Query Match 55.7%; Score 12.8; DB 6; Length 27;
Best Local Similarity 87.5%; Pred. No. 9.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 acgtgtgcggtcctca 17
||||| ||||| |||||
DB 8 ACCTGTGCGGTCTCA 23

RESULT 8
AX069493/c AX069493 27 bp DNA PAT 25-JAN-2001
LOCUS AX069493
DEFINITION Sequence 157 from Patent WO0102600.
ACCESSION AX069493
VERSION AX069493.1 GI:12579278
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 27)
AUTHORS Yuan,C.S.
TITLE Detection of analytes using attenuated enzymes
JOURNAL Patent: WO 0102600-A 157 11-JAN-2001;
GENERAL ATOMICS (US)
FEATURES
source Location/Qualifiers
1..27
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotides for producing SAM hydrolase
mutants"

BASE COUNT 6 a 8 c 9 g 4 t

ORIGIN

Query Match 55.7%; Score 12.8; DB 6; Length 27;
Best Local Similarity 87.5%; Pred. No. 9.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 gtgcggtcctcagaga 21
||||| ||||| |||||
DB 20 GTGCTGTCTCTCAGAGA 5

RESULT 9
AX069494 AX069494 27 bp DNA PAT 25-JAN-2001
LOCUS AX069494
DEFINITION Sequence 158 from Patent WO0102600.
ACCESSION AX069494
VERSION AX069494.1 GI:12579279
KEYWORDS
SOURCE synthetic construct.

```
ORGANISM    synthetic construct
REFERENCE    1 (bases 1 to 27)
AUTHORS      Yuan,C.S.
TITLE        Detection of analytes using attenuated enzymes
JOURNAL      Patent: WO 0102600-A 158 11-JAN-2001;
              GENERAL ATOMICS (US)
FEATURES     Location/Qualifiers
             source
               1..27
               /organism="synthetic construct"
               /db_xref="taxon:32630"
               /note="Oligonucleotides for producing SAM hydrolase
               mutants"
BASE COUNT   4 a          9 c          8 g          6 t
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Query Match  55.7%; Score 12.8; DB 6; Length 27;
Best Local Similarity 87.5%; Pred. No. 9.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 gtgcggtcctcagaga 21
    ||| ||||| |||||
Db 8 GTGCTGCTCAGAGA 23

RESULT 10
LOCUS       U33690             59 bp      DNA          VRT          15-JUN-2001
DEFINITION Hypentelium nigrificans 28S ribosomal RNA gene, partial sequence.
ACCESSION   U33690
VERSION     U33690.1 GI:2443963
KEYWORDS
SOURCE      Hypentelium nigrificans.
            Hypentelium nigrificans
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
            Cypriniformes; Catostomidae; Hypentelium.
REFERENCE   1 (bases 1 to 59)
AUTHORS     Dimmick,W.W. and Larson,A.
TITLE       A molecular and morphological perspective on the phylogenetic
            relationships of the otophysan fishes
JOURNAL     Mol. Phylogenet. Evol. 6 (1), 120-133 (1996)
MEDLINE     96426866
PUBMED      8812312
REFERENCE   2 (bases 1 to 59)
AUTHORS     Dimmick,W.W. and Larson,A.
TITLE       Direct Submission
JOURNAL     Submitted (10-AUG-1995) University of Kansas, Dyché Hall, Jayhawk
            Boulevard, Lawrence, KS 66045, USA
FEATURES     Location/Qualifiers
             source
               1..59
               /organism="Hypentelium nigrificans"
               /db_xref="taxon:61316"
               /tissue_type="muscle"
               /note="CT2854"
             <1..>59
             /product="28S ribosomal RNA"
BASE COUNT   7 a          24 c          21 g          7 t
ORIGIN
Query Match  55.7%; Score 12.8; DB 5; Length 59;
Best Local Similarity 87.5%; Pred. No. 8.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aacggtgcggtcctc 16
    ||||| ||||| |||||
Db 53 AACGTGGCGGTCGCC 38

RESULT 11
AX159789/c

ORGANISM    AX159789          51 bp      DNA          PAT          22-JUN-2001
DEFINITION Sequence 3117 from Patent WO0140521.
ACCESSION   AX159789
VERSION     AX159789.1 GI:14541120
KEYWORDS
SOURCE      human.
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 51)
AUTHORS     Shimkets,R.A. and Leach,M.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL     Patent: WO 0140521-A 3117 07-JUN-2001;
            Curagen Corporation (US)
FEATURES     Location/Qualifiers
             source
               1..51
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
             misc_feature
               26
               /note="1 of 2 allelic variants (3118 is other entry)
               Accession number cg42919304"
BASE COUNT   22 a          8 c          18 g          3 t
ORIGIN
Query Match  54.8%; Score 12.6; DB 6; Length 51;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 gtgtcggtcctcagagac 22
    ||||| ||||| |||||
Db 41 GTTGGCTCTCCTCAGAGC 23

RESULT 12
LOCUS       AR118184           60 bp      DNA          PAT          16-MAY-2001
DEFINITION Sequence 29 from patent US 6140490.
ACCESSION   AR118184
VERSION     AR118184.1 GI:14099090
KEYWORDS
SOURCE      Unknown.
            Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 60)
AUTHORS     Biesecker,G. and Gold,L.
TITLE       High affinity nucleic acid ligands of complement system proteins
JOURNAL     Patent: US 6140490-A 29 31-OCT-2000;
            Location/Qualifiers
FEATURES     source
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               /organism="unknown"
BASE COUNT   12 a          18 c          18 g          12 t
ORIGIN
Query Match  54.8%; Score 12.6; DB 6; Length 60;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 aacggtgcggtcctcaga 19
    ||| | ||||| |||||
Db 30 AACGTTGGCGGTCGTCAGA 48

RESULT 13
LOCUS       I01529/c           60 bp      ss-DNA          PAT          21-MAY-1993
DEFINITION Sequence 4 from Patent US 4816565.
ACCESSION   I01529
VERSION     I01529.1 GI:269966
KEYWORDS
SOURCE      Unknown.
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